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RAW SEQUENCE LISTING DATE: 08/30/2004
 PATENT APPLICATION: US/10/777,521 TIME: 14:45:54

Input Set : N:\Crf3\RULE60\10777521.raw.txt
 Output Set: N:\CRF4\08302004\J777521.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:
 2 (i) APPLICANT: Adema, Gosse Jan
 3 Meygaard, Linde
 4 Gorman, Daniel M.
 5 McClanahan, Terrill K.
 6 Zurawski, Sandra M.
 7 Zurawski, Gerard
 8 Lanier, Lewis L.
 9 Phillips Jr., Joseph H.
 10 (ii) TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
 11 Related Reagents
 12 (iii) NUMBER OF SEQUENCES: 22
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: DNAX Research Institute
 15 (B) STREET: 901 California Avenue
 16 (C) CITY: Palo Alto
 17 (D) STATE: California
 18 (E) COUNTRY: USA
 19 (F) ZIP: 94304-1104
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Floppy disk
 22 (B) COMPUTER: IBM PC compatible
 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 25 (vi) CURRENT APPLICATION DATA:
 C--> 26 (A) APPLICATION NUMBER: US/10/777,521
 C--> 27 (B) FILING DATE: 11-Feb-2004
 28 (vii) PRIOR APPLICATION DATA:
 W--> 29 (A) APPLICATION NUMBER: US/09/546,049
 30 (B) FILING DATE: 10-Apr-2000
 W--> 31 (A) APPLICATION NUMBER: US/08/985,950
 32 (B) FILING DATE: 05-DEC-1997
 W--> 33 (A) APPLICATION NUMBER: US 60/041,279
 34 (B) FILING DATE: 21-MARCH-1997
 W--> 35 (A) APPLICATION NUMBER: US 60/033,181
 36 (B) FILING DATE: 16-DEC-1996
 W--> 37 (A) APPLICATION NUMBER: US 60/032,252
 38 (B) FILING DATE: 06-DEC-1996
 39 (viii) ATTORNEY/AGENT INFORMATION:
 40 (A) NAME: Ching, Edwin P.
 41 (B) REGISTRATION NUMBER: 34,090
 42 (C) REFERENCE/DOCKET NUMBER: DX0670K

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43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: (650)852-9196
45 (B) TELEFAX: (650)496-1204
46 (2) INFORMATION FOR SEQ ID NO: 1:
47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 1249 base pairs
49 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
51 (D) TOPOLOGY: linear
52 (ii) MOLECULE TYPE: cDNA
53 (ix) FEATURE:
54 (A) NAME/KEY: CDS
55 (B) LOCATION: 154..1062
56 (ix) FEATURE:
57 (A) NAME/KEY: mat_peptide
58 (B) LOCATION: 211..1062
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60 GTTTGGGGGAA GGCTCCTGGC CCCCACAGCC CTCTTCGGAG CCTGAGCCCG GCTCTCCTCA 60
61 CTCACCTCAA CCCCCAGGCG GCCCCTCCAC AGGGCCCCCTC TCCTGCCTGG ACGGCTCTGC 120
62 TGGTCTCCCC GTCCCCTGGA GAAGAACAAG GCC ATG GGT CGG CCC CTG CTG CTG 174
63 Met Gly Arg Pro Leu Leu Leu
64 -19 -15
65 CCC CTA CTG CCC CTG CTG CTG CCG CCA GCA TTT CTG CAG CCT AGT GGC 222
66 Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly
67 -10 -5 1
68 TCC ACA GGA TCT GGT CCA AGC TAC CTT TAT GGG GTC ACT CAA CCA AAA 270
69 Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys
70 5 10 15 20
71 CAC CTC TCA GCC TCC ATG GGT GGC TCT GTG GAA ATC CCC TTC TCC TTC 318
72 His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe
73 25 30 35
74 TAT TAC CCC TGG GAG TTA GCC ACA GCT CCC GAC GTG AGA ATA TCC TGG 366
75 Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp
76 40 45 50
77 AGA CGG GGC CAC TTC CAC GGG CAG TCC TTC TAC AGC ACA AGG CCG CCT 414
78 Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro
79 55 60 65
80 TCC ATT CAC AAG GAT TAT GTG AAC CGG CTC TTT CTG AAC TGG ACA GAG 462
81 Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu
82 70 75 80
83 GGT CAG AAG AGC GGC TTC CTC AGG ATC TCC AAC CTG CAG AAG CAG GAC 510
84 Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp
85 85 90 95 100
86 CAG TCT GTG TAT TTC TGC CGA GTT GAG CTG GAC ACA CGG AGC TCA GGG 558
87 Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly
88 105 110 115
89 AGG CAG CAG TGG CAG TCC ATC GAG GGG ACC AAA CTC TCC ATC ACC CAG 606
90 Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln
91 120 125 130

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92  GCT GTC ACG ACC ACC ACC CAG AGG CCC AGC AGC ATG ACT ACC ACC TGG      654
93  Ala Val Thr Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp
94      135                      140                      145
95  AGG CTC AGT AGC ACA ACC ACC ACA ACC GGC CTC AGG GTC ACA CAG GGC      702
96  Arg Leu Ser Ser Thr Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly
97      150                      155                      160
98  AAA CGA CGC TCA GAC TCT TGG CAC ATA AGT CTG GAG ACT GCT GTG GGG      750
99  Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly
100     165                      170                      175                      180
101  GTG GCA GTG GCT GTC ACT GTG CTC GGA ATC ATG ATT TTG GGA CTG ATC      798
102  Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile
103      185                      190                      195
104  TGC CTC CTC AGG TGG AGG AGA AGG AAA GGT CAG CAG CGG ACT AAA GCC      846
105  Cys Leu Leu Arg Trp Arg Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala
106      200                      205                      210
107  ACA ACC CCA GCC AGG GAA CCC TTC CAA AAC ACA GAG GAG CCA TAT GAG      894
108  Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu
109      215                      220                      225
110  AAT ATC AGG AAT GAA GGA CAA AAT ACA GAT CCC AAG CTA AAT CCC AAG      942
111  Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys
112      230                      235                      240
113  GAT GAC GGC ATC GTA TAT GCT TCC CTT GCC CTC TCC AGC TCC ACC TCA      990
114  Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser
115      245                      250                      255                      260
116  CCC AGA GCA CCT CCC AGC CAC CGT CCC CTC AAG AGC CCC CAG AAC GAG      1038
117  Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
118      265                      270                      275
119  ACC CTG TAC TCT GTC TTA AAG GCC TAACCAATGG ACAGCCCTCT CAAGACTGAA      1092
120  Thr Leu Tyr Ser Val Leu Lys Ala
121      280
122  TGGTGAGGCC AGGTACAGTG GCGCACACCT GTAATCCCAG CTACTCTGAA GCCTGAGGCA      1152
123  GAATCAAGTG AGCCCAGGAG TTCAGGGCCA GCTTTGATAA TGGAGCGAGA TGCCATCTCT      1212
124  AGTTAAAAAT ATATATTAAC AATAAAGTAA CAAATTT      1249
126 (2) INFORMATION FOR SEQ ID NO: 2:
127     (i) SEQUENCE CHARACTERISTICS:
128         (A) LENGTH: 303 amino acids
129         (B) TYPE: amino acid
130         (D) TOPOLOGY: linear
131     (ii) MOLECULE TYPE: protein
132     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
133  Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu Pro Pro
134  -19          -15          -10          -5
135  Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
136      1          5          10
137  Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
138      15          20          25
139  Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
140      30          35          40          45
141  Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser

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142           50           55           60
143 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
144           65           70           75
145 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
146           80           85           90
147 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
148           95          100          105
149 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
150          110          115          120          125
151 Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro
152           130          135          140
153 Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr
154           145          150          155
155 Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
156           160          165          170
157 Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
158           175          180          185
159 Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
160          190          195          200          205
161 Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
162           210          215          220
163 Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
164           225          230          235
165 Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
166           240          245          250
167 Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
168           255          260          265
169 Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
170          270          275          280

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172 (2) INFORMATION FOR SEQ ID NO: 3:

173 (i) SEQUENCE CHARACTERISTICS:

174 (A) LENGTH: 376 base pairs

175 (B) TYPE: nucleic acid

176 (C) STRANDEDNESS: single

177 (D) TOPOLOGY: linear

178 (ii) MOLECULE TYPE: cDNA

179 (ix) FEATURE:

180 (A) NAME/KEY: CDS

181 (B) LOCATION: 78..374

182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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183 CCCAGTGTC CCTAGACAGA GCATCCTTGC CTTCTGATG GCTTTGCTGA TCTCGCTTCC      60
184 CTGGAGGGGAC TCCAGCC ATG GCT CAG GTC CTG CTT CTG CTC TCA TCA GGC      110
185           Met Ala Gln Val Leu Leu Leu Ser Ser Gly
186           1           5           10
187 TGT CTG CAT GCT GGA AAT TCA GAA AGA TAC AAC AGA AAA AAT GGC TTT      158
188 Cys Leu His Ala Gly Asn Ser Glu Arg Tyr Asn Arg Lys Asn Gly Phe
189           15           20           25
190 GGG GTC AAC CAA CCT GAA CGC TGC TCT GGA GTC CAG GGT GGC TCC ATC      206
191 Gly Val Asn Gln Pro Glu Arg Cys Ser Gly Val Gln Gly Gly Ser Ile

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192          30          35          40
193  GAC ATC CCC TTC TCC TTC TAT TTC CCC TGG AAG TTG GCC AAG GAT CCA      254
194  Asp Ile Pro Phe Ser Phe Tyr Phe Pro Trp Lys Leu Ala Lys Asp Pro
195          45          50          55
196  CAG ATG AGC ATA GCC TGG AAA TGG AAG GAT TTC CAT GGG GAA GTC ATC      302
197  Gln Met Ser Ile Ala Trp Lys Trp Lys Asp Phe His Gly Glu Val Ile
198          60          65          70          75
199  TAC AAC TCC TCC CTG CCT TTC ATA CAT GAG CAC TTC AAG GGC CGG CTC      350
200  Tyr Asn Ser Ser Leu Pro Phe Ile His Glu His Phe Lys Gly Arg Leu
201          80          85          90
202  ATC CTG AAC TGG ACA CAG GGT CAG AC      376
203  Ile Leu Asn Trp Thr Gln Gly Gln
204          95
206 (2) INFORMATION FOR SEQ ID NO: 4:
207   (i) SEQUENCE CHARACTERISTICS:
208       (A) LENGTH: 99 amino acids
209       (B) TYPE: amino acid
210       (D) TOPOLOGY: linear
211   (ii) MOLECULE TYPE: protein
212   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
213  Met Ala Gln Val Leu Leu Leu Leu Ser Ser Gly Cys Leu His Ala Gly
214    1          5          10          15
215  Asn Ser Glu Arg Tyr Asn Arg Lys Asn Gly Phe Gly Val Asn Gln Pro
216          20          25          30
217  Glu Arg Cys Ser Gly Val Gln Gly Gly Ser Ile Asp Ile Pro Phe Ser
218          35          40          45
219  Phe Tyr Phe Pro Trp Lys Leu Ala Lys Asp Pro Gln Met Ser Ile Ala
220          50          55          60
221  Trp Lys Trp Lys Asp Phe His Gly Glu Val Ile Tyr Asn Ser Ser Leu
222          65          70          75          80
223  Pro Phe Ile His Glu His Phe Lys Gly Arg Leu Ile Leu Asn Trp Thr
224          85          90          95
225  Gln Gly Gln
227 (2) INFORMATION FOR SEQ ID NO: 5:
228   (i) SEQUENCE CHARACTERISTICS:
229       (A) LENGTH: 1279 base pairs
230       (B) TYPE: nucleic acid
231       (C) STRANDEDNESS: single
232       (D) TOPOLOGY: linear
233   (ii) MOLECULE TYPE: cDNA
234   (ix) FEATURE:
235       (A) NAME/KEY: CDS
236       (B) LOCATION: 155..1015
237   (ix) FEATURE:
238       (A) NAME/KEY: misc_feature
239       (B) LOCATION: 1247
240       (D) OTHER INFORMATION: /note= "nucleotide 1247 designated
241  C, but may be C or T"
242   (ix) FEATURE:

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10777521.raw.txt

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L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:31 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:33 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:37 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)